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	215	220	225
Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu			
	230	235	240
Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr			
	245	250	255
Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly			
	260	265	270
Arg Lys Lys Thr Ser Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe			
	275	280	285
Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro			
	290	295	300
Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu			
	305	310	315
Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser			
	320	325	330
Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val			
	335	340	345
Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln			
	350	355	360
Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro Arg Arg Ala			
	365	370	375
Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile Ser Trp Arg			
	380	385	390
Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp Ala Val Pro			
	395	400	405

Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys Pro Asp Val
410 415 420
Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr Asp Tyr Lys
425 430 435
5 Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser Ser Pro Val
440 445 450
Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg
455 460 465
Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro
470 475 480
Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro
485 490 495
Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val
500 505 510
15 Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr
515 520 525
Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu
530 535 540
Ile Gly Arg Lys Lys Thr Ser
20 545

SEQ. ID No. 14

LENGTH: 826

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5	Ala	Ala	Ser	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile	Gly	Pro	Asp	
					5					10					15	
	Thr	Met	Arg	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile	Asp	Leu	Thr	
					20					25					30	
	Asn	Phe	Leu	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu	Glu	Asp	Val	
					35					40					45	
10	Ala	Glu	Leu	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr	
					50					55					60	
	Asn	Leu	Leu	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	
					65					70					75	
	Tyr	Glu	Gln	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	
15					80					85					90	
	Gly	Leu	Asp	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	
					95					100					105	
	Asn	Ser	Phe	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	
					110					115					120	
20	Gly	Tyr	Arg	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	
					125					130					135	
	Arg	Glu	Asp	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	
					140					145					150	
	Asn	Leu	Thr	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	
25					155					160					165	

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Asn	Gly	Arg	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr
				170					175					180
Val	Ser	Asp	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro
				185					190					195
Thr	Ser	Leu	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg
				200					205					210
Tyr	Tyr	Arg	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val
				215					220					225
Gln	Glu	Phe	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser
				230					235					240
Gly	Leu	Lys	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val
				245					250					255
Thr	Gly	Arg	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro	Ile	Ser	Ile
				260					265					270
Asn	Tyr	Arg	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Thr	Ser	Ala	Ile	Pro
				275					280					285
Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu
				290					295					300
Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg
				305					310					315
Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile
				320					325					330
Asn	Leu	Ala	Pro	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met
				335					340					345
Val	Ala	Thr	Lys	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr

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	350	355	360
Leu Thr Ser Arg Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn			
	365	370	375
Val Ser Pro Pro Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr			
	380	385	390
Thr Ile Thr Ile Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly			
	395	400	405
Phe Gln Val Asp Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln			
	410	415	420
Arg Thr Ile Lys Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu			
	425	430	435
Gln Pro Gly Thr Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp			
	440	445	450
Asn Ala Arg Ser Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile			
	455	460	465
Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser			
	470	475	480
Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr			
	485	490	495
Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val			
	500	505	510
Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu			
	515	520	525
Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn			
	530	535	540

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Asn	Gln	Lys	Ser	Glu	Pro	Leu	Ile	Gly	Arg	Lys	Lys	Thr	Ser	Ala
				545					550					555
Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr
				560					565					570
Ser	Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly
				575					580					585
Tyr	Arg	Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys
				590					595					600
Glu	Ile	Asn	Leu	Ala	Pro	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly
				605					610					615
Leu	Met	Val	Ala	Thr	Lys	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys
				620					625					630
Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu
				635					640					645
Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr
				650					655					660
Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile
				665					670					675
Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro
				680					685					690
Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr
				695					700					705
Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu
				710					715					720
Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	Thr

	725	730	735
	Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe Leu Ala Thr Thr Pro		
	740	745	750
	Asn Ser Leu Leu Val Ser Trp Gln Pro Pro Arg Ala Arg Ile Thr		
5	755	760	765
	Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly Ser Pro Pro Arg Glu		
	770	775	780
	Val Val Pro Arg Pro Arg Pro Gly Val Thr Glu Ala Thr Ile Thr		
	785	790	795
	Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile Tyr Val Ile Ala Leu		
	800	805	810
	Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile Gly Arg Lys Lys Thr		
	815	820	825
	Ser		

SEQ. ID No. 15

LENGTH: 38

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCGCT ATTCCTGCAC CAACTGAC

38

SEQ. ID No. 16

LENGTH: 36

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

5 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAAGGATCCC TAACTAGTCT TTTTCCTTCC AATCAG 36

SEQ. ID No. 17

LENGTH: 1644

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an
artificial polypeptide)

15 SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCGGGTG 120
ACCCCCAAGG AGAAGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240
20 GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTACCA CTCTGGAGAA TGTCAGCCCA 300
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAACC 360
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTTC CAGCCAATGG CCAGACTCCA 420
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540

ATCGACGCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTTCCTGGC CACCACACCC 600
AATTCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660
TATGAGAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGGCCCGCCC TGGTGTCACA 720
GAGGCTACTA TTACTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780
5 AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCCTGCA 840
CCAAGTACC TGAAGTTCAC TCAGGTCACA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900
CCCAATGTTT AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080
10 CAGGGTGTTG TCACCACTCT GGAGAATGTC AGCCCACCAA GAAGGGCTCG TGTGACAGAT 1140
GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260
GTCAGAAGCT ACACCATCAC AGGTTTACAA CCAGGCACTG ACTACAAGAT CTACCTGTAC 1320
ACCTTGAATG ACAATGCTCG GAGCTCCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380
15 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CCTTGCTGGT ATCATGGCAG 1440
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAAGCCTGG GTCTCCTCCC 1500
AGAGAAGTGG TCCCTCGGCC CCGCCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560
CCGGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620
CTGATTGGAA GGAAAAAGAC TAGT 1644

20 SEQ. ID No. 18

LENGTH: 37

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

25 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCCCC ACTGACCTGC GATTCAC

37

SEQ. ID No. 19

LENGTH: 38

5 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

10 AAAAGATCTC TAACTAGTGG ATGGTTTGTC AATTTCTG

38

SEQ. ID No. 20

LENGTH: 2481

TYPE: nucleic acid

STRANDEDNESS: double

15 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGGCAGCTA GCCCCACTGA CCTGCGATTC ACCAACATTG GTCCAGACAC CATGCGTGTC 60

20 ACCTGGGCTC CACCCCCATC CATTGATTTA ACCAACTTCC TGGTGCGTTA CTCACCTGTG 120

AAAAATGAGG AAGATGTTGC AGAGTTGTCA ATTTCTCCTT CAGACAATGC AGTGGTCTTA 180

ACAAATCTCC TGCCTGGTAC AGAATATGTA GTGAGTGTCT CCAGTGTCTA CGAACAACAT 240

GAGAGCACAC CTCTTAGAGG AAGACAGAAA ACAGGTCTTG ATTCCCCAAC TGGCATTGAC 300

TTTTCTGATA TTACTGCCAA CTCTTTTACT GTGCACTGGA TTGCTCCTCG AGCCACCATC 360
ACTGGCTACA GGATCCGCCA TCATCCCGAG CACTTCAGTG GGAGACCTCG AGAAGATCGG 420
GTGCCCCACT CTCGGAATTC CATCACCTC ACCAACCTCA CTCCAGGCAC AGAGTATGTG 480
GTCAGCATCG TTGCTCTTAA TGGCAGAGAG GAAAGTCCCT TATTGATTGG CCAACAATCA 540
5 ACAGTTTCTG ATGTTCCGAG GGACCTGGAA GTTGTGCTG CGACCCCCAC CAGCCTACTG 600
ATCAGCTGGG ATGCTCCTGC TGTCACAGTG AGATATTACA GGATCACTTA CGGAGAAACA 660
GGAGGAAATA GCCCTGTCCA GGAGTTCCT GTGCCTGGGA GCAAGTCTAC AGCTACCATC 720
AGCGGCCTTA AACCTGGAGT TGATTATACC ATCACTGTGT ATGCTGTCAC TGGCCGTGGA 780
GACAGCCCCG CAAGCAGCAA GCCAATTTC ATTAATTACC GAACAGAAAT TGACAAACCA 840
10 TCCACTAGCG CTATTCCTGC ACCAACTGAC CTGAAGTTCA CTCAGGTCAC ACCCACAAGC 900
CTGAGCGCCC AGTGGACACC ACCCAATGTT CAGCTCACTG GATATCGAGT GCGGGTGACC 960
CCCAAGGAGA AGACCGGACC AATGAAAGAA ATCAACCTTG CTCCTGACAG CTCATCCGTG 1020
GTTGTATCAG GACTTATGGT GGCCACCAA TATGAAGTGA GTGTCTATGC TCTTAAGGAC 1080
ACTTTGACAA GCAGACCAGC TCAGGGTGTT GTCACCACTC TGGAGAATGT CAGCCCACCA 1140
15 AGAAGGGCTC GTGTGACAGA TGCTACTGAG ACCACCATCA CCATTAGCTG GAGAACCAAG 1200
ACTGAGACGA TCACTGGCTT CCAAGTTGAT GCCGTTCCAG CCAATGGCCA GACTCCAATC 1260
CAGAGAACCA TCAAGCCAGA TGTCAGAAGC TACACCATCA CAGGTTTACA ACCAGGCACT 1320
GACTACAAGA TCTACCTGTA CACCTTGAAT GACAATGCTC GGAGCTCCCC TGTGGTCATC 1380
GACGCCTCCA CTGCCATTGA TGCACCATCC AACCTGCGTT TCCTGGCCAC CACACCCAAT 1440
20 TCCTTGCTGG TATCATGGCA GCCGCCACGT GCCAGGATTA CCGGCTACAT CATCAAGTAT 1500
GAGAAGCCTG GGTCTCCTCC CAGAGAAGTG GTCCCTCGGC CCCGCCCTGG TGTCACAGAG 1560
GCTACTATTA CTGGCCTGGA ACCGGGAACC GAATATACAA TTTATGTCAT TGCCCTGAAG 1620
AATAATCAGA AGAGCGAGCC CCTGATTGGA AGGAAAAAGA CTAGCGCTAT TCCTGCACCA 1680
ACTGACCTGA AGTTCACTCA GGTCACACCC ACAAGCCTGA GCGCCCAGTG GACACCACCC 1740
25 AATGTTCAGC TCACTGGATA TCGAGTGCGG GTGACCCCCA AGGAGAAGAC CGGACCAATG 1800

AAAGAAATCA ACCTTGCTCC TGACAGCTCA TCCGTGGTTG TATCAGGACT TATGGTGGCC 1960
ACCAAATATG AAGTGAGTGT CTATGCTCTT AAGGACACTT TGACAAGCAG ACCAGCTCAG 1920
GGTGTGTGCA CCACTCTGGA GAATGTCAGC CCACCAAGAA GGGCTCGTGT GACAGATGCT 1980
ACTGAGACCA CCATCACCAT TAGCTGGAGA ACCAAGACTG AGACGATCAC TGGCTTCCAA 2040
5 GTTGATGCCG TTCCAGCCAA TGGCCAGACT CCAATCCAGA GAACCATCAA GCCAGATGTC 2100
AGAAGCTACA CCATCACAGG TTTACAACCA GGCCTGACT ACAAGATCTA CCTGTACACC 2160
TTGAATGACA ATGCTCGGAG CTCCCCTGTG GTCATCGACG CCTCCACTGC CATTGATGCA 2220
CCATCCAACC TGCCTTTTCCT GGCCACCACA CCCAATTCCT TGCTGGTATC ATGGCAGCCG 2280
CCACGTGCCA GGATTACCGG CTACATCATC AAGTATGAGA AGCCTGGGTC TCCTCCCAGA 2340
10 GAAGTGGTCC CTCGGCCCCG CCCTGGTGTC ACAGAGGCTA CTATTACTGG CCTGGAACCG 2400
GGAACCGAAT ATACAATTTA TGTCATTGCC CTGAAGAATA ATCAGAAGAG CGAGCCCCTG 2460
ATTGGAAGGA AAAAGACTAG T 2481

SEQ. ID No. 21

LENGTH: 472

15 TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

20 Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
1 5 10 15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 25 30
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

		35		40		45									
	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr	Asn	Leu	Leu
		50		55		60									
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln
5		65		70		75									
	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp
		80		85		90									
	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe
		95		100		105									
10	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg
		110		115		120									
	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	Arg	Glu	Asp
		125		130		135									
	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	Asn	Leu	Thr
15		140		145		150									
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	Asn	Gly	Arg
		155		160		165									
	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr	Val	Ser	Asp
		170		175		180									
20	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro	Thr	Ser	Leu
		185		190		195									
	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr	Tyr	Arg
		200		205		210									
	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu	Phe
25		215		220		225									

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410 415 420
Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr
425 430 435
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser
5 440 445 450
Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser
455 460 465
Asn Leu Arg Phe Leu Ala Thr
470

10 SEQ. ID No. 22

LENGTH: 457

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
1 5 10 15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 20 25 30
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 40 45
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu
50 55 60

	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln	
						65				70					75	
	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp	
						80				85					90	
5	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe	
						95				100					105	
	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg	
						110				115					120	
	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	Arg	Glu	Asp	
						125				130					135	
	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	Asn	Leu	Thr	
						140				145					150	
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	Asn	Gly	Arg	
						155				160					165	
15	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr	Val	Ser	Asp	
						170				175					180	
	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro	Thr	Ser	Leu	
						185				190					195	
	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr	Tyr	Arg	
20						200				205					210	
	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu	Phe	
						215				220					225	
	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys	
						230				235					240	
25	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Thr	Gly	Arg	

		245		250		255									
	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro	Ile	Ser	Ile	Asn	Tyr	Arg
		260		265		270									
	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Met	Asn	Val	Ser	Pro	Pro	Arg	Arg
5		275		280		285									
	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp
		290		295		300									
	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val
		305		310		315									
10	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp
		320		325		330									
	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr
		335		340		345									
	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro
15		350		355		360									
	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser	Asn	Leu
		365		370		375									
	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser	Trp	Gln
		380		385		390									
20	Pro	Pro	Arg	Ala	Arg	Ile	Thr	Gly	Tyr	Ile	Ile	Lys	Tyr	Glu	Lys
		395		400		405									
	Pro	Gly	Ser	Pro	Pro	Arg	Glu	Val	Val	Pro	Arg	Pro	Arg	Pro	Gly
		410		415		420									
	Val	Thr	Glu	Ala	Thr	Ile	Thr	Gly	Leu	Glu	Pro	Gly	Thr	Glu	Tyr
25		425		430		435									

Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro
440 445 450
Leu Ile Gly Arg Lys Lys Thr
455

5 SEQ. ID No. 23

LENGTH: 549

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

10 MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg

1 5 10 15

Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu

15 20 25 30

Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu

35 40 45

Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu

50 55 60

20 Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln

65 70 75

His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp

80 85 90

Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe

	95	100	105
	Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg		
	110	115	120
	Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp		
5	125	130	135
	Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr		
	140	145	150
	Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg		
	155	160	165
10	Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp		
	170	175	180
	Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu		
	185	190	195
	Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg		
15	200	205	210
	Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe		
	215	220	225
	Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys		
	230	235	240
20	Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg		
	245	250	255
	Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg		
	260	265	270
	Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp		
25	275	280	285

	Leu	Lys	Phe	Thr	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp
					290					295					300
	Thr	Pro	Pro	Asn	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr
					305					310					315
5	Pro	Lys	Glu	Lys	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro
					320					325					330
	Asp	Ser	Ser	Ser	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys
					335					340					345
	Tyr	Glu	Val	Ser	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg
					350					355					360
	Pro	Ala	Gln	Gly	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro
					365					370					375
	Arg	Arg	Ala	Arg	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile
					380					385					390
15	Ser	Trp	Arg	Thr	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp
					395					400					405
	Ala	Val	Pro	Ala	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys
					410					415					420
	Pro	Asp	Val	Arg	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr
20					425					430					435
	Asp	Tyr	Lys	Ile	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser
					440					445					450
	Ser	Pro	Val	Val	Ile	Asp	Ala	Ser	Thr	Ala	Ile	Asp	Ala	Pro	Ser
					455					460					465
25	Asn	Leu	Arg	Phe	Leu	Ala	Thr	Thr	Pro	Asn	Ser	Leu	Leu	Val	Ser

470 475 480
Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr
485 490 495
Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg
5 500 505 510
Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr
515 520 525
Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser
530 535 540
10 Glu Pro Leu Ile Gly Arg Lys Lys Thr
545

SEQ. ID No. 24

LENGTH: 574

TYPE: amino acid

15 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
20 1 5 10 15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 25 30
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 40 45

	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr	Asn	Leu	Leu	
					50					55						60
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln	
					65					70						75
5	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp	
					80					85						90
	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe	
					95					100						105
	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg	
10					110					115						120
	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	Arg	Glu	Asp	
					125					130						135
	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	Asn	Leu	Thr	
					140					145						150
15	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	Asn	Gly	Arg	
					155					160						165
	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr	Val	Ser	Asp	
					170					175						180
	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro	Thr	Ser	Leu	
20					185					190						195
	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr	Tyr	Arg	
					200					205						210
	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu	Phe	
					215					220						225
25	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys	

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	230	235	240
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg			
	245	250	255
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg			
	260	265	270
Thr Glu Ile Asp Lys Pro Ser Met Ala Ile Pro Ala Pro Thr Asp			
	275	280	285
Leu Lys Phe Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp			
	290	295	300
Thr Pro Pro Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr			
	305	310	315
Pro Lys Glu Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro			
	320	325	330
Asp Ser Ser Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys			
	335	340	345
Tyr Glu Val Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg			
	350	355	360
Pro Ala Gln Gly Val Val Thr Thr Leu Glu Asn Val Ser Pro Pro			
	365	370	375
Arg Arg Ala Arg Val Thr Asp Ala Thr Glu Thr Thr Ile Thr Ile			
	380	385	390
Ser Trp Arg Thr Lys Thr Glu Thr Ile Thr Gly Phe Gln Val Asp			
	395	400	405
Ala Val Pro Ala Asn Gly Gln Thr Pro Ile Gln Arg Thr Ile Lys			
	410	415	420

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Pro Asp Val Arg Ser Tyr Thr Ile Thr Gly Leu Gln Pro Gly Thr
      425                      430                      435
Asp Tyr Lys Ile Tyr Leu Tyr Thr Leu Asn Asp Asn Ala Arg Ser
      440                      445                      450
5  Ser Pro Val Val Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser
      455                      460                      465
Asn Leu Arg Phe Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser
      470                      475                      480
Trp Gln Pro Pro Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr
      485                      490                      495
10 Glu Lys Pro Gly Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg
      500                      505                      510
Pro Gly Val Thr Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr
      515                      520                      525
15 Glu Tyr Thr Ile Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser
      530                      535                      540
Glu Pro Leu Ile Gly Arg Lys Lys Thr Asp Glu Leu Pro Gln Leu
      545                      550                      555
20 Val Thr Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp
      560                      565                      570
Val Pro Ser Thr

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SEQ. ID No. 25

LENGTH: 274

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

5 Pro Thr Asp Leu Arg Phe Thr Asn Ile Gly Pro Asp Thr Met Arg
1 5 10 15
Val Thr Trp Ala Pro Pro Pro Ser Ile Asp Leu Thr Asn Phe Leu
20 25 30
Val Arg Tyr Ser Pro Val Lys Asn Glu Glu Asp Val Ala Glu Leu
35 40 45
Ser Ile Ser Pro Ser Asp Asn Ala Val Val Leu Thr Asn Leu Leu
50 55 60
Pro Gly Thr Glu Tyr Val Val Ser Val Ser Ser Val Tyr Glu Gln
65 70 75
15 His Glu Ser Thr Pro Leu Arg Gly Arg Gln Lys Thr Gly Leu Asp
80 85 90
Ser Pro Thr Gly Ile Asp Phe Ser Asp Ile Thr Ala Asn Ser Phe
95 100 105
Thr Val His Trp Ile Ala Pro Arg Ala Thr Ile Thr Gly Tyr Arg
20 110 115 120
Ile Arg His His Pro Glu His Phe Ser Gly Arg Pro Arg Glu Asp
125 130 135
Arg Val Pro His Ser Arg Asn Ser Ile Thr Leu Thr Asn Leu Thr
140 145 150
25 Pro Gly Thr Glu Tyr Val Val Ser Ile Val Ala Leu Asn Gly Arg

155 160 165
Glu Glu Ser Pro Leu Leu Ile Gly Gln Gln Ser Thr Val Ser Asp
170 175 180
Val Pro Arg Asp Leu Glu Val Val Ala Ala Thr Pro Thr Ser Leu
5 185 190 195
Leu Ile Ser Trp Asp Ala Pro Ala Val Thr Val Arg Tyr Tyr Arg
200 205 210
Ile Thr Tyr Gly Glu Thr Gly Gly Asn Ser Pro Val Gln Glu Phe
215 220 225
10 Thr Val Pro Gly Ser Lys Ser Thr Ala Thr Ile Ser Gly Leu Lys
230 235 240
Pro Gly Val Asp Tyr Thr Ile Thr Val Tyr Ala Val Thr Gly Arg
245 250 255
Gly Asp Ser Pro Ala Ser Ser Lys Pro Ile Ser Ile Asn Tyr Arg
15 260 265 270
Thr Glu Ile Asp

SEQ. ID No. 26

LENGTH: 1374

TYPE: nucleic acid

20 STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGCCCCACTG ACCTGCGATT CACCAACATT GGTCCAGACA CCATGCGTGT CACCTGGGCT 60
CCACCCCCAT CCATTGATTT AACCAACTTC CTGGTGCGTT ACTCACCTGT GAAAAATGAG 120
GAAGATGTTG CAGAGTTGTC AATTTCTCCT TCAGACAATG CAGTGGTCTT AACAAATCTC 180
CTGCCTGGTA CAGAATATGT AGTGAGTGTC TCCAGTGTCT ACGAACAACA TGAGAGCACA 240
5 CCTCTTAGAG GAAGACAGAA AACAGGTCTT GATTCCCCAA CTGGCATTGA CTTTTCTGAT 300
ATTACTGCCA ACTCTTTTAC TGTGCACTGG ATTGCTCCTC GAGCCACCAT CACTGGCTAC 360
AGGATCCGCC ATCATCCCGA GCACTTCAGT GGGAGACCTC GAGAAGATCG GGTGCCCCAC 420
TCTCGGAATT CCATCACCTT CACCAACCTC ACTCCAGGCA CAGAGTATGT GGTCAGCATC 480
GTTGCTCTTA ATGGCAGAGA GGAAAGTCCC TTATTGATTG GCCAACAATC AACAGTTTCT 540
10 GATGTTCCGA GGGACCTGGA AGTTGTTGCT GCGACCCCCA CCAGCCTACT GATCAGCTGG 600
GATGCTCCTG CTGTCACAGT GAGATATTAC AGGATCACTT ACGGAGAAAC AGGAGGAAAT 660
AGCCCTGTCC AGGAGTTCAC TGTGCCTGGG AGCAAGTCTA CAGCTACCAT CAGCGGCCTT 720
AAACCTGGAG TTGATTATAC CATCACTGTG TATGCTGTCA CTGGCCGTGG AGACAGCCCC 780
GCAAGCAGCA AGCCAATTTT CATTAATTAC CGAACAGAAA TTGACAAACC ATCCATGGCA 840
15 GCCGGGAGCA TCACCACGCT GCCCGCCTTG CCCGAGGATG GCGGCAGCGG CGCCTTCCCG 900
CCCGGCCACT TCAAGGACCC CAAGCGGCTG TACTGCAAAA ACGGGGGCTT CTTCTTGCGC 960
ATCCACCCCG ACGGCCGAGT TGACGGGGTC CGGGAGAAGA GCGACCCTCA CATCAAGCTA 1020
CAACTTCAAG CAGAAGAGAG AGGAGTTGTG TCTATCAAAG GAGTGTGTGC TAACCGTTAC 1080
CTGGCTATGA AGGAAGATGG AAGATTACTG GCTTCTAAAT GTGTTACGGA TGAGTGT TTC 1140
20 TTTTTTGAAC GATTGGAATC TAATAACTAC AATACTTACC GCTCAAGGAA ATACACCAGT 1200
TGGTATGTGG CACTGAAACG AACTGGGCAG TATAAACTTG GATCCAAAAC AGGACCTGGG 1260
CAGAAAGCTA TACTTTTTCT TCCAATGTCT GCTGCTAGCG ACGAGCTTCC CCAACTGGTA 1320
ACCCTTCCAC ACCCCAATCT TCATGGACCA GAGATCTTGG ATGTTCTTTC CACA 1374

LENGTH: 1416

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

5 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

10
15
20
25

CCCACTGACC TGCGATTACAC CAACATTGGT CCAGACACCA TGCCTGTCAC CTGGGCTCCA 60
CCCCCATCCA TTGATTTAAC CAACTTCCTG GTGCGTTACT CACCTGTGAA AAATGAGGAA 120
GATGTTGCAG AGTTGTCAAT TTCTCCTTCA GACAATGCAG TGGTCTTAAC AAATCTCCTG 180
CCTGGTACAG AATATGTAGT GAGTGTCTCC AGTGTCTACG AACAACATGA GAGCACACCT 240
CTTAGAGGAA GACAGAAAAC AGGTCTTGAT TCCCCAACTG GCATTGACTT TTCTGATATT 300
ACTGCCAACT CTTTTACTGT GCACTGGATT GCTCCTCGAG CCACCATCAC TGGCTACAGG 360
ATCCGCCATC ATCCCGAGCA CTTCACTGGG AGACCTCGAG AAGATCGGGT GCCCCACTCT 420
CGGAATTCCA TCACCCTCAC CAACCTCACT CCAGGCACAG AGTATGTGGT CAGCATCGTT 480
GCTCTTAATG GCAGAGAGGA AAGTCCCTTA TTGATTGGCC AACAATCAAC AGTTTCTGAT 540
GTTCCGAGGG ACCTGGAAGT TGTTGCTGCG ACCCCCACCA GCCTACTGAT CAGCTGGGAT 600
GCTCCTGCTG TCACAGTGAG ATATTACAGG ATCACTTACG GAGAAACAGG AGGAAATAGC 660
CCTGTCCAGG AGTTCACTGT GCCTGGGAGC AAGTCTACAG CTACCATCAG CGGCCTTAAA 720
CCTGGAGTTG ATTATACCAT CACTGTGTAT GCTGTCACTG GCCGTGGAGA CAGCCCCGCA 780
AGCAGCAAGC CAATTTCCAT TAATTACCGA ACAGAAATTG ACAAACCATC CATGGCTATT 840
CCTGCACCAA CTGACCTGAA GTTCACTCAG GTCACACCCA CAAGCCTGAG CGCCCAGTGG 900
ACACCACCCA ATGTTTCAGCT CACTGGATAT CGAGTGCGGG TGACCCCCAA GGAGAAGACC 960
GGACCAATGA AAGAAATCAA CCTTGCTCCT GACAGCTCAT CCGTGGTTGT ATCAGGACTT 020
ATGGTGGCCA CCAAATATGA AGTGAGTGTC TATGCTCTTA AGGACACTTT GACAAGCAGA 1080

CCAGCTCAGG GTGTTGTCAC CACTCTGGAG AATGTCAGCC CACCAAGAAG GGCTCGTGTG 1140
 ACAGATGCTA CTGAGACCAC CATCACCATT AGCTGGAGAA CCAAGACTGA GACGATCACT 1200
 GGCTTCCAAG TTGATGCCGT TCCAGCCAAT GGCCAGACTC CAATCCAGAG AACCATCAAG 1260
 CCAGATGTCA GAAGCTACAC CATCACAGGT TTACAACCAG GCACTGACTA CAAGATCTAC 1320
 5 CTGTACACCT TGAATGACAA TGCTCGGAGC TCCCCTGTGG TCATCGACGC CTCCACTGCC 1380
 ATTGATGCAC CATCCAACCT GCGTTTCCTG GCCACC 1416

SEQ. ID No. 28

LENGTH: 35

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Gly Gly Arg Gly Thr Pro Gly Lys Pro Gly Pro Arg Gly Gln Arg
 15 1 5 10 15
 Gly Pro Thr Gly Pro Arg Gly Glu Arg Gly Pro Arg Gly Ile Thr
 20 25 30
 Gly Lys Pro Gly Pro
 35

SEQ. ID No. 29

LENGTH: 302

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

	Pro	Thr	Asp	Leu	Arg	Phe	Thr	Asn	Ile	Gly	Pro	Asp	Thr	Met	Arg	
5	1				5					10					15	
	Val	Thr	Trp	Ala	Pro	Pro	Pro	Ser	Ile	Asp	Leu	Thr	Asn	Phe	Leu	
					20					25					30	
	Val	Arg	Tyr	Ser	Pro	Val	Lys	Asn	Glu	Glu	Asp	Val	Ala	Glu	Leu	
					35					40					45	
10	Ser	Ile	Ser	Pro	Ser	Asp	Asn	Ala	Val	Val	Leu	Thr	Asn	Leu	Leu	
					50					55					60	
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Val	Ser	Ser	Val	Tyr	Glu	Gln	
					65					70					75	
	His	Glu	Ser	Thr	Pro	Leu	Arg	Gly	Arg	Gln	Lys	Thr	Gly	Leu	Asp	
15					80					85					90	
	Ser	Pro	Thr	Gly	Ile	Asp	Phe	Ser	Asp	Ile	Thr	Ala	Asn	Ser	Phe	
					95					100					105	
	Thr	Val	His	Trp	Ile	Ala	Pro	Arg	Ala	Thr	Ile	Thr	Gly	Tyr	Arg	
					110					115					120	
20	Ile	Arg	His	His	Pro	Glu	His	Phe	Ser	Gly	Arg	Pro	Arg	Glu	Asp	
					125					130					135	
	Arg	Val	Pro	His	Ser	Arg	Asn	Ser	Ile	Thr	Leu	Thr	Asn	Leu	Thr	
					140					145					150	
	Pro	Gly	Thr	Glu	Tyr	Val	Val	Ser	Ile	Val	Ala	Leu	Asn	Gly	Arg	
25					155					160					165	

	Glu	Glu	Ser	Pro	Leu	Leu	Ile	Gly	Gln	Gln	Ser	Thr	Val	Ser	Asp
					170					175					180
	Val	Pro	Arg	Asp	Leu	Glu	Val	Val	Ala	Ala	Thr	Pro	Thr	Ser	Leu
					185					190					195
5	Leu	Ile	Ser	Trp	Asp	Ala	Pro	Ala	Val	Thr	Val	Arg	Tyr	Tyr	Arg
					200					205					210
	Ile	Thr	Tyr	Gly	Glu	Thr	Gly	Gly	Asn	Ser	Pro	Val	Gln	Glu	Phe
					215					220					225
	Thr	Val	Pro	Gly	Ser	Lys	Ser	Thr	Ala	Thr	Ile	Ser	Gly	Leu	Lys
					230					235					240
	Pro	Gly	Val	Asp	Tyr	Thr	Ile	Thr	Val	Tyr	Ala	Val	Thr	Gly	Arg
					245					250					255
	Gly	Asp	Ser	Pro	Ala	Ser	Ser	Lys	Pro	Ile	Ser	Ile	Asn	Tyr	Arg
					260					265					270
15	Thr	Glu	Ile	Asp	Lys	Pro	Ser	Asp	Glu	Leu	Pro	Gln	Leu	Val	Thr
					275					280					285
	Leu	Pro	His	Pro	Asn	Leu	His	Gly	Pro	Glu	Ile	Leu	Asp	Val	Pro
					290					295					300
	Ser	Thr													

20 SEQ. ID No. 30

LENGTH: 573

TYPE: amino acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

	Met	Ala	Ala	Ser	Ala	Ile	Pro	Ala	Pro	Thr	Asp	Leu	Lys	Phe	Thr	
					5					10						15
5	Gln	Val	Thr	Pro	Thr	Ser	Leu	Ser	Ala	Gln	Trp	Thr	Pro	Pro	Asn	
					20					25						30
	Val	Gln	Leu	Thr	Gly	Tyr	Arg	Val	Arg	Val	Thr	Pro	Lys	Glu	Lys	
					35					40						45
	Thr	Gly	Pro	Met	Lys	Glu	Ile	Asn	Leu	Ala	Pro	Asp	Ser	Ser	Ser	
10					50					55						60
	Val	Val	Val	Ser	Gly	Leu	Met	Val	Ala	Thr	Lys	Tyr	Glu	Val	Ser	
					65					70						75
	Val	Tyr	Ala	Leu	Lys	Asp	Thr	Leu	Thr	Ser	Arg	Pro	Ala	Gln	Gly	
					80					85						90
15	Val	Val	Thr	Thr	Leu	Glu	Asn	Val	Ser	Pro	Pro	Arg	Arg	Ala	Arg	
					95					100						105
	Val	Thr	Asp	Ala	Thr	Glu	Thr	Thr	Ile	Thr	Ile	Ser	Trp	Arg	Thr	
					110					115						120
	Lys	Thr	Glu	Thr	Ile	Thr	Gly	Phe	Gln	Val	Asp	Ala	Val	Pro	Ala	
20					125					130						135
	Asn	Gly	Gln	Thr	Pro	Ile	Gln	Arg	Thr	Ile	Lys	Pro	Asp	Val	Arg	
					140					145						150
	Ser	Tyr	Thr	Ile	Thr	Gly	Leu	Gln	Pro	Gly	Thr	Asp	Tyr	Lys	Ile	
					155					160						165
25	Tyr	Leu	Tyr	Thr	Leu	Asn	Asp	Asn	Ala	Arg	Ser	Ser	Pro	Val	Val	

	170	175	180
	Ile Asp Ala Ser Thr Ala Ile Asp Ala Pro Ser Asn Leu Arg Phe		
	185	190	195
	Leu Ala Thr Thr Pro Asn Ser Leu Leu Val Ser Trp Gln Pro Pro		
5	200	205	210
	Arg Ala Arg Ile Thr Gly Tyr Ile Ile Lys Tyr Glu Lys Pro Gly		
	215	220	225
	Ser Pro Pro Arg Glu Val Val Pro Arg Pro Arg Pro Gly Val Thr		
	230	235	240
10	Glu Ala Thr Ile Thr Gly Leu Glu Pro Gly Thr Glu Tyr Thr Ile		
	245	250	255
	Tyr Val Ile Ala Leu Lys Asn Asn Gln Lys Ser Glu Pro Leu Ile		
	260	265	270
	Gly Arg Lys Lys Thr Ala Ile Pro Ala Pro Thr Asp Leu Lys Phe		
	275	280	285
	Thr Gln Val Thr Pro Thr Ser Leu Ser Ala Gln Trp Thr Pro Pro		
	290	295	300
	Asn Val Gln Leu Thr Gly Tyr Arg Val Arg Val Thr Pro Lys Glu		
	305	310	315
20	Lys Thr Gly Pro Met Lys Glu Ile Asn Leu Ala Pro Asp Ser Ser		
	320	325	330
	Ser Val Val Val Ser Gly Leu Met Val Ala Thr Lys Tyr Glu Val		
	335	340	345
	Ser Val Tyr Ala Leu Lys Asp Thr Leu Thr Ser Arg Pro Ala Gln		
25	350	355	360

25

545 550 555
Leu Pro His Pro Asn Leu His Gly Pro Glu Ile Leu Asp Val Pro
560 565 570
Ser Thr Ser

5 SEQ. ID No. 31

LENGTH: 37

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

10 MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

AAACCATGGC AGCTAGCAAT GTCAGCCCAC CAAGAAG 37

SEQ. ID No. 32

LENGTH: 37

15 TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

20 AAAGGATCCC TAACTAGTGG AAGGAACATC CAAGATC 37

SEQ. ID No. 33

LENGTH: 1722

TYPE: nucleic acid

STRANDEDNESS: double

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGGCAGCTA GCGCTATTCC TGCACCAACT GACCTGAAGT TCACTCAGGT CACACCCACA 60
AGCCTGAGCG CCCAGTGGAC ACCACCCAAT GTTCAGCTCA CTGGATATCG AGTGCGGGTG 120
ACCCCCAAGG AGAAGACCGG ACCAATGAAA GAAATCAACC TTGCTCCTGA CAGCTCATCC 180
GTGGTTGTAT CAGGACTTAT GGTGGCCACC AAATATGAAG TGAGTGTCTA TGCTCTTAAG 240
GACACTTTGA CAAGCAGACC AGCTCAGGGT GTTGTACCA CTCTGGAGAA TGTCAGCCCA 300
CCAAGAAGGG CTCGTGTGAC AGATGCTACT GAGACCACCA TCACCATTAG CTGGAGAACC 360
AAGACTGAGA CGATCACTGG CTTCCAAGTT GATGCCGTTT CAGCCAATGG CCAGACTCCA 420
ATCCAGAGAA CCATCAAGCC AGATGTCAGA AGCTACACCA TCACAGGTTT ACAACCAGGC 480
ACTGACTACA AGATCTACCT GTACACCTTG AATGACAATG CTCGGAGCTC CCCTGTGGTC 540
ATCGACGCCT CCACTGCCAT TGATGCACCA TCCAACCTGC GTTTCCTGGC CACCACACCC 600
AATTCCTTGC TGGTATCATG GCAGCCGCCA CGTGCCAGGA TTACCGGCTA CATCATCAAG 660
TATGAGAAGC CTGGGTCTCC TCCCAGAGAA GTGGTCCCTC GGCCCCGCC TGGTGTCA 720
GAGGCTACTA TTACTGGCCT GGAACCGGGA ACCGAATATA CAATTTATGT CATTGCCCTG 780
AAGAATAATC AGAAGAGCGA GCCCCTGATT GGAAGGAAAA AGACTAGCGC TATTCCTGCA 840
CCAAGTACC TGAAGTTCAC TCAGGTCACA CCCACAAGCC TGAGCGCCCA GTGGACACCA 900
CCCAATGTTC AGCTCACTGG ATATCGAGTG CGGGTGACCC CCAAGGAGAA GACCGGACCA 960
ATGAAAGAAA TCAACCTTGC TCCTGACAGC TCATCCGTGG TTGTATCAGG ACTTATGGTG 1020
GCCACCAAAT ATGAAGTGAG TGTCTATGCT CTTAAGGACA CTTTGACAAG CAGACCAGCT 1080
CAGGGTGTTG TCACCACTCT GGAGAATGTC AGCCCACCAA GAAGGGCTCG TGTGACAGAT 1140

GCTACTGAGA CCACCATCAC CATTAGCTGG AGAACCAAGA CTGAGACGAT CACTGGCTTC 1200
CAAGTTGATG CCGTTCCAGC CAATGGCCAG ACTCCAATCC AGAGAACCAT CAAGCCAGAT 1260
GTCAGAAGCT ACACCATCAC AGGTTTACAA CCAGGCACTG ACTACAAGAT CTACCTGTAC 1320
ACCTTGAATG ACAATGCTCG GAGCTCCCCT GTGGTCATCG ACGCCTCCAC TGCCATTGAT 1380
5 GCACCATCCA ACCTGCGTTT CCTGGCCACC ACACCCAATT CCTTGCTGGT ATCATGGCAG 1440
CCGCCACGTG CCAGGATTAC CGGCTACATC ATCAAGTATG AGAAGCCTGG GTCTCCTCCC 1500
AGAGAAGTGG TCCCTCGGCC CCGCCCTGGT GTCACAGAGG CTACTATTAC TGGCCTGGAA 1560
CCGGGAACCG AATATACAAT TTATGTCATT GCCCTGAAGA ATAATCAGAA GAGCGAGCCC 1620
CTGATTGGAA GGAAAAAGAC TAGCGACGAG CTTCCCCAAC TGGTAACCCT TCCACACCCC 1680
10 AATCTTCATG GACCAGAGAT CTTGGATGTT CCTTCCACTA GT 1722

SEQ. ID No. 34

LENGTH: 412

TYPE: amino acid

STRANDEDNESS: single

15 TOPOLOGY: linear

MOLECULAR TYPE: peptide

SEQUENCE:

Met Ser Pro Ile Leu Gly Tyr Trp Lys Ile Lys Gly Leu Val Gln

5 10 15

20 Pro Thr Arg Leu Leu Leu Glu Tyr Leu Glu Glu Lys Tyr Glu Glu

20 25 30

His Leu Tyr Glu Arg Asp Glu Gly Asp Lys Trp Arg Asn Lys Lys

35 40 45

Phe Glu Leu Gly Leu Glu Phe Pro Asn Leu Pro Tyr Tyr Ile Asp

		50		55		60									
	Gly	Asp	Val	Lys	Leu	Thr	Gln	Ser	Met	Ala	Ile	Ile	Arg	Tyr	Ile
		65		70		75									
	Ala	Asp	Lys	His	Asn	Met	Leu	Gly	Gly	Cys	Pro	Lys	Glu	Arg	Ala
5		80		85		90									
	Glu	Ile	Ser	Met	Leu	Glu	Gly	Ala	Val	Leu	Asp	Ile	Arg	Tyr	Gly
		95		100		105									
	Val	Ser	Arg	Ile	Ala	Tyr	Ser	Lys	Asp	Phe	Glu	Thr	Leu	Lys	Val
		110		115		120									
10	Asp	Phe	Leu	Ser	Lys	Leu	Pro	Glu	Met	Leu	Lys	Met	Phe	Glu	Asp
		125		130		135									
	Arg	Leu	Cys	His	Lys	Thr	Tyr	Leu	Asn	Gly	Asp	His	Val	Thr	His
		140		145		150									
	Pro	Asp	Phe	Met	Leu	Tyr	Asp	Ala	Leu	Asp	Val	Val	Leu	Tyr	Met
15		155		160		165									
	Asp	Pro	Met	Cys	Leu	Asp	Ala	Phe	Pro	Lys	Leu	Val	Cys	Phe	Lys
		170		175		180									
	Lys	Arg	Ile	Glu	Ala	Ile	Pro	Gln	Ile	Asp	Lys	Tyr	Leu	Lys	Ser
		185		190		195									
20	Ser	Lys	Tyr	Ile	Ala	Trp	Pro	Leu	Gln	Gly	Trp	Gln	Ala	Thr	Phe
		200		205		210									
	Gly	Gly	Gly	Asp	His	Pro	Pro	Lys	Ser	Asp	Leu	Ile	Glu	Gly	Arg
		215		220		225									
	Gly	Ile	Pro	Arg	Asn	Ser	Gly	Ala	Pro	Pro	Arg	Leu	Ile	Cys	Asp
25		230		235		240									

Ser Arg Val Leu Gln Arg Tyr Leu Leu Glu Ala Lys Glu Ala Glu
245 250 255
Asn Ile Thr Thr Gly Cys Ala Glu His Cys Ser Leu Asn Glu Asn
260 265 270
5 Ile Thr Val Pro Asp Thr Lys Val Asn Phe Tyr Ala Trp Lys Arg
275 280 285
Met Glu Val Gly Gln Gln Ala Val Glu Val Trp Gln Gly Leu Ala
290 295 300
Leu Leu Ser Glu Ala Val Leu Arg Gly Gln Ala Leu Leu Val Asn
305 310 315
Ser Ser Gln Pro Trp Glu Pro Leu Gln Leu His Val Asp Lys Ala
320 325 330
Val Ser Gly Leu Arg Ser Leu Thr Thr Leu Leu Arg Ala Leu Gly
335 340 345
15 Ala Gln Lys Glu Ala Ile Ser Pro Pro Asp Ala Ala Ser Ala Ala
350 355 360
Pro Leu Arg Thr Ile Thr Ala Asp Thr Phe Arg Lys Leu Phe Arg
365 370 375
Val Tyr Ser Asn Phe Leu Arg Gly Lys Leu Lys Leu Tyr Thr Gly
380 385 390
20 Glu Ala Cys Arg Thr Gly Asp Arg Leu Ala Met Asp Pro Leu Glu
395 400 405
Ser Thr Arg Ala Ala Ala Ser
410

SEQ. ID No. 35

LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

5 TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GCTCCCTCTG GGCCTCCCAG TCCT

24

SEQ. ID No. 36

10 LENGTH: 24

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

15 SEQUENCE:

GTTGGTGAGG GAGGTGGTGG ATAT

24

SEQ. ID No. 37

LENGTH: 33

TYPE: nucleic acid

20 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

GGCCTCCCGA ATTCCGGTGC CCCACCACGC CTC

33

SEQ. ID No. 38

LENGTH: 33

TYPE: nucleic acid

5 STRANDEDNESS: single

TOPOLOGY: linear

MOLECULAR TYPE: other nucleic acid (synthetic DNA)

SEQUENCE:

CCCACGTGGA TCCATGGCTA ATCTGTCCCC TGT

33

10 SEQ. ID No. 39

LENGTH: 1239

TYPE: nucleic acid

STRANDEDNESS: single

TOPOLOGY: linear

15 MOLECULAR TYPE: other nucleic acid (DNA encoding an artificial polypeptide)

SEQUENCE:

ATGTCCCCTA TACTAGGTTA TTGGAAAATT AAGGGCCTTG TGCAACCCAC TCGACTTCTT 60
TTGGAATATC TTGAAGAAAA ATATGAAGAG CATTTGTATG AGCGCGATGA AGGTGATAAA 120
20 TGGCGAAACA AAAAGTTTGA ATTGGGTTTG GAGTTTCCCA ATCTTCCTTA TTATATTGAT 180
GGTGATGTTA AATTAACACA GTCTATGGCC ATCATACGTT ATATAGCTGA CAAGCACAAC 240
ATGTTGGGTG GTTGTCCAAA AGAGCGTGCA GAGATTTCAA TGCTTGAAGG AGCGGTTTTG 300
GATATTAGAT ACGGTGTTTC GAGAATTGCA TATAGTAAAG ACTTTGAAAC TCTCAAAGTT 360

GATTTTCTTA GCAAGCTACC TGAAATGCTG AAAATGTTCG AAGATCGTTT ATGTCATAAA 420
ACATATTTAA ATGGTGATCA TGTAACCCAT CCTGACTTCA TGTGTATGA CGCTCTTGAT 480
GTTGTTTTAT ACATGGACCC AATGTGCCTG GATGCGTTCC CAAAATTAGT TTGTTTTAAA 540
AAACGTATTG AAGCTATCCC ACAAATTGAT AAGTACTTGA AATCCAGCAA GTATATAGCA 600
5 TGGCCTTTGC AGGGCTGGCA AGCCACGTTT GGTGGTGGCG ACCATCCTCC AAAATCGGAT 660
CTGATCGAAG GTCGTGGGAT CCCCAGGAAT TCCGGTGCCC CACCACGCCT CATCTGTGAC 720
AGCCGAGTCC TGCAGAGGTA CCTCTTGGAG GCCAAGGAGG CCGAGAATAT CACGACGGGC 780
TGTGCTGAAC ACTGCAGCTT GAATGAGAAT ATCACTGTCC CAGACACCAA AGTTAATTTT 840
TATGCCTGGA AGAGGATGGA GGTCGGGCAG CAGGCCGTAG AAGTCTGGCA GGGCCTGGCC 900
10 CTGCTGTCGG AAGCTGTCCT GCGGGGCCAG GCCCTGTTGG TCAACTCTTC CCAGCCGTGG 960
GAGCCCCTGC AGCTGCATGT GGATAAAGCC GTCAGTGGCC TTCGCAGCCT CACCACTCTG 1020
CTTCGGGCTC TGGGAGCCCA GAAGGAAGCC ATCTCCCCTC CAGATGCGGC CTCAGCTGCT 1080
CCACTCCGAA CAATCACTGC TGACACTTTC CGAAACTCT TCCGAGTCTA CTCCAATTTT 1140
CTCCGGGGAA AGCTGAAGCT GTACACAGGG GAGGCCTGCA GGACAGGGGA CAGATTAGCC 1200
15 ATGGATCCTC TAGAGTCGAC TCGAGCGGCC GCATCGTGA 1239